

400 MHz ¹³C NMR spectrum of 1

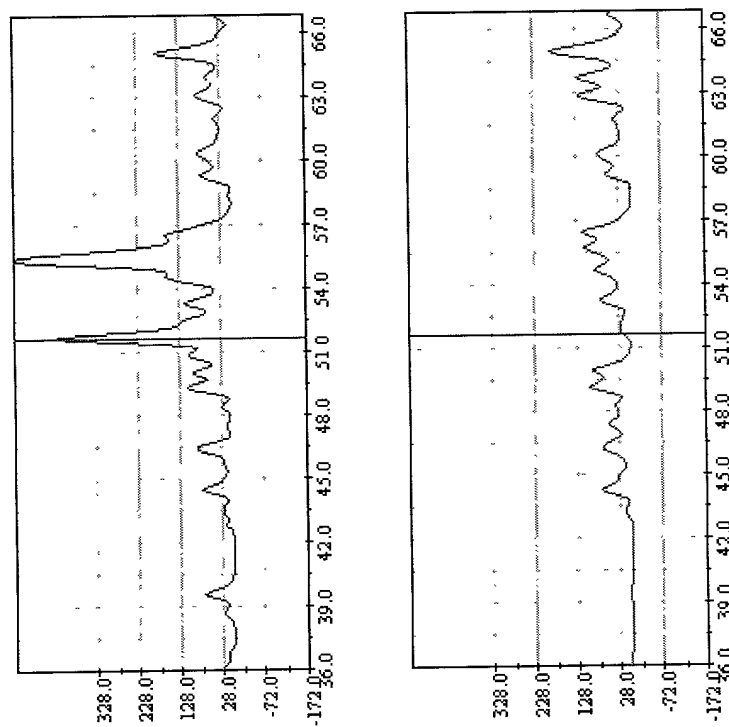


Figure 1

W0h051-7.Seq x Cjlp181r.Seq..

; GAP of: W0h051-7.Seq check: 6926 from: 1 to: 52

seq of dicamba induced band w0c0 51.7

to: Cjlp181r.Seq check: 2737 from: 1 to: 714

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Nwsgapdna.Cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	520	Length:	714
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

W0h051-7.Seq x Cjlp181r.Seq..

1gctagctgcgcggtgaccacgcat	26
1	CGATCGAAGTGGGTGTGTGCTAGCTAGCTAGCTGCGCCGTGACCGACACAT	50
27	gaccgcagtgcgcggggctgatca.....	52
51	GACCGCAGTGCGCGGGGGCTGATCAAGGAAAGTATCGGATGGAGCTG	100

Figure 2

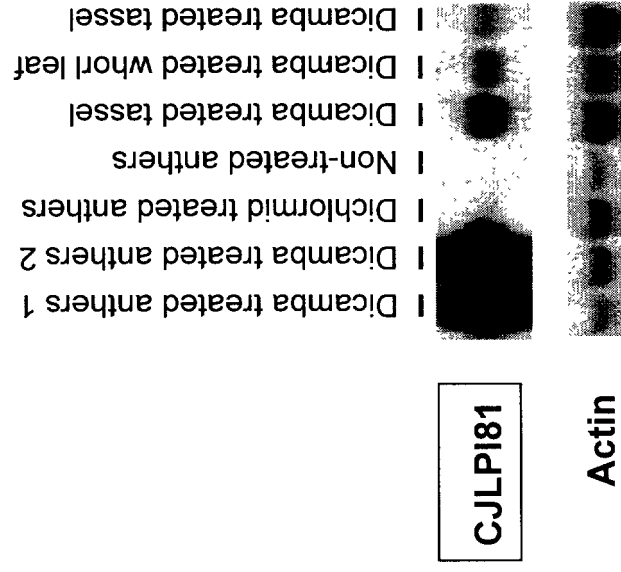


Figure 3

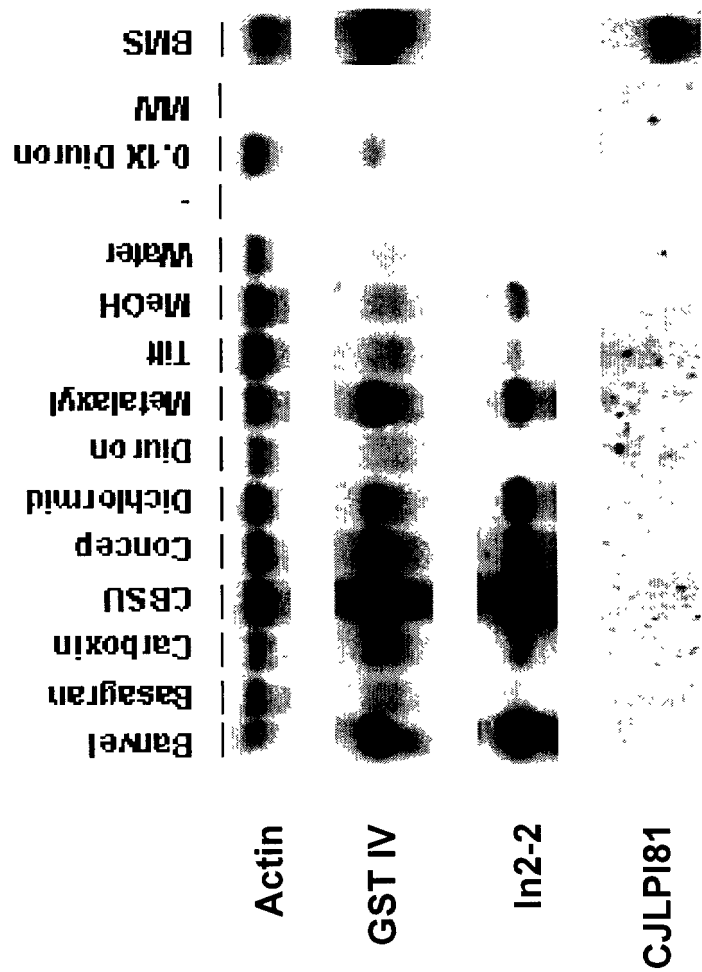


Figure 4

DOMAIN I NLS

ZmAxig1 1 MELELGLAPPNP HQPLAAAAEFVGLLSSSAGSCGNKRVLGDAFGAAKAAT 50
 || || || | : | : || : |||
 PS-IAA4/5 1 mefkate lrlgl.pg.....iteeeekkiihgssvvknnkr..... 36

51 LPLFVCEGDGGGDRDRDGVVDHEQQSNNVPRKKRLVGWPPVKARRRS 100
 | : | : | | | : | | : ||||| : | : |
 35 qlpqtseesvsiskvtndehi.vessaaapakaki vgwppirsyrkns 84

101CGGYVKV KLEGVPIGRKVDVSIHGSYQELLRTLESMPSGNQD 145
 || : ||| : : | | || : : | | || : ||. || :
 85 lheadvgg i fvkvsmdgapylrkidlrvyggy sellkaletmfkl.tige 133
 β α α

146 HAEDEVVSHERRRHPYVVTYEDGEDWLLVGDDVPWEVFKSVKRLKI 195
 :. | | | | | : ||| : ||| : ||| :. || | ||| : |
 134 yseregykgse.....yapt yedkdgdwmlvg.dvpwdfvtsckrlri 176

196 LA..... 197
 :
 177 mkgteakg lgcgv 189

Figure 5

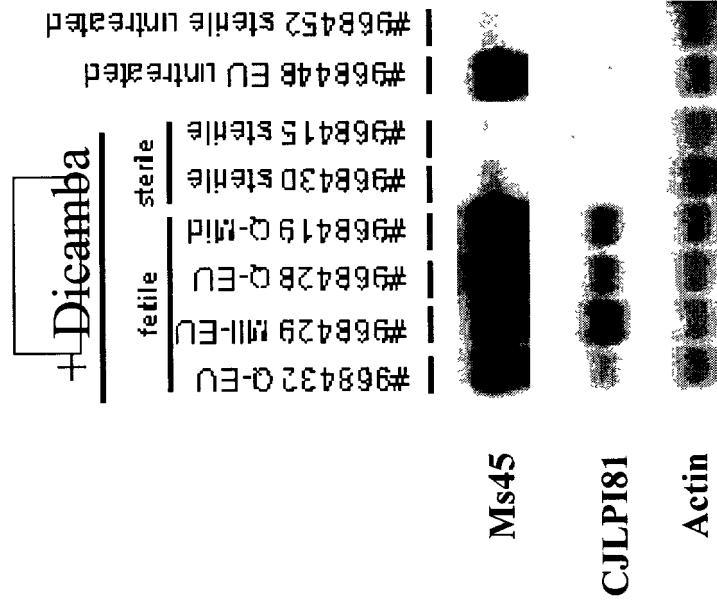


Figure 6

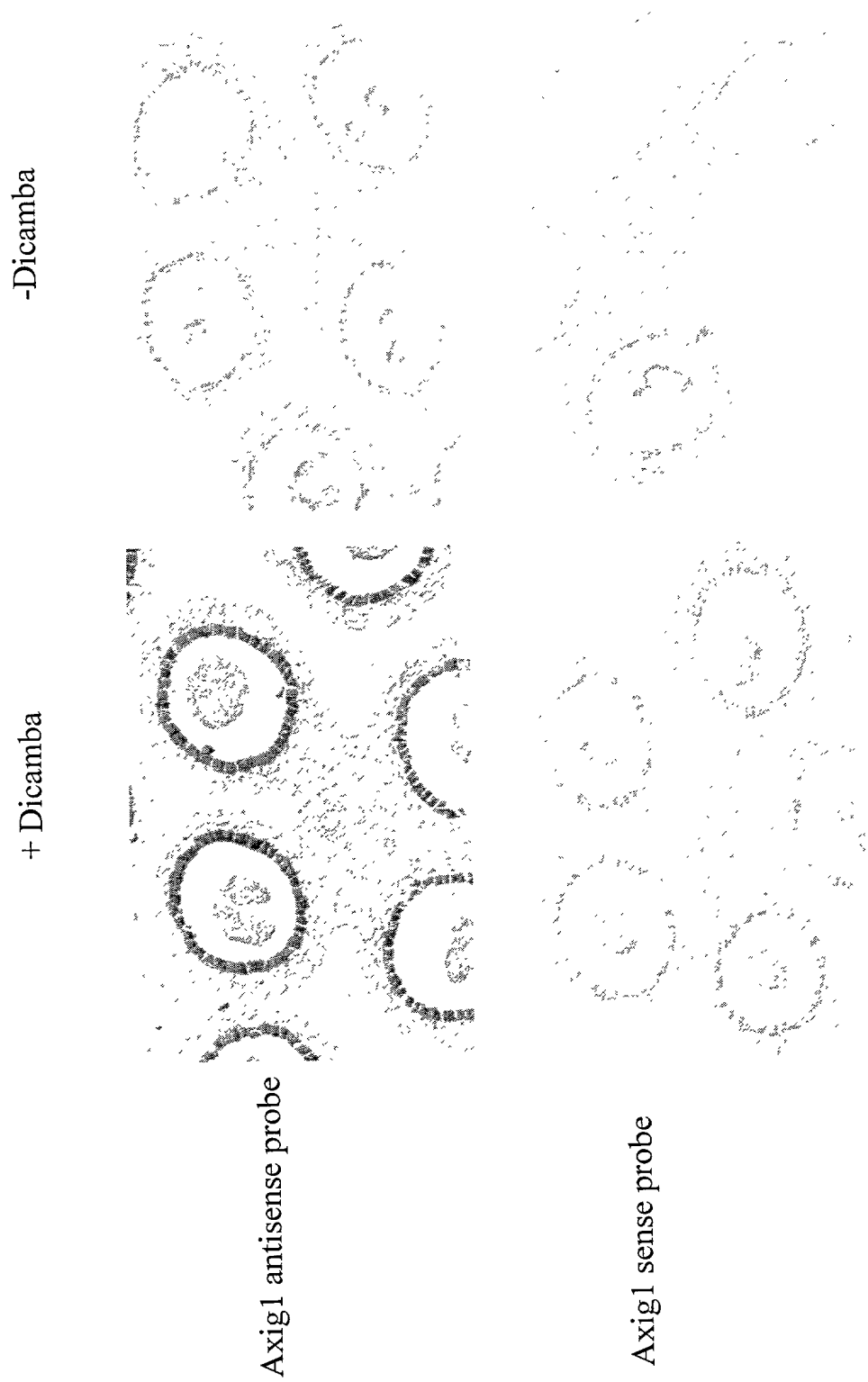


Figure 7

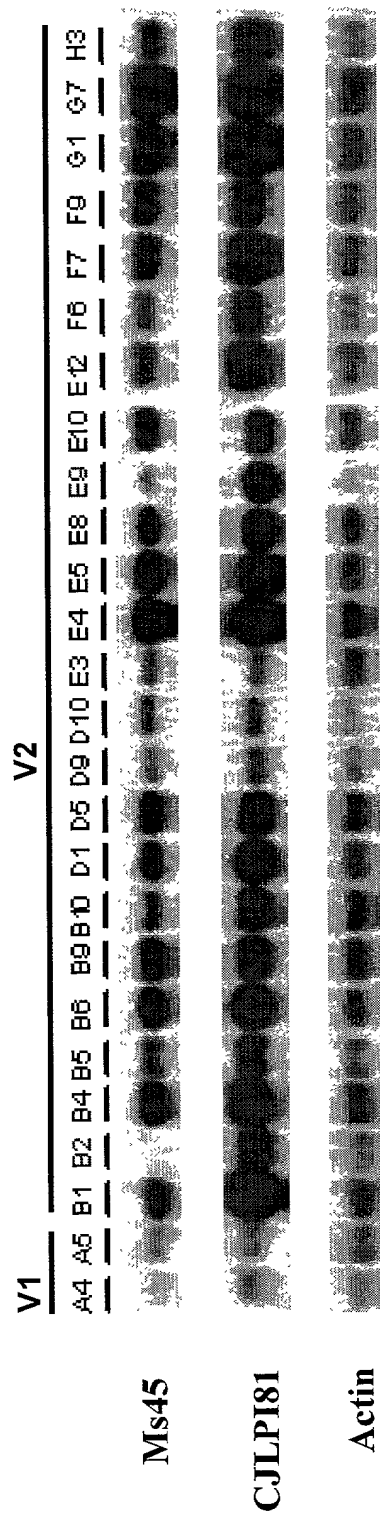


Figure 8

Figure 9

GAP of: Czaal47.Seq check: 446 from: 1 to: 1214
to: Axiglcomplete.Con check: 928 from: 1 to: 3123

Symbol comparison table:
Gencoredisk: [Gcgcore.Data.Rundata]Nwsgapdna.Cmp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 10871 Length: 3123
Ratio: 8.955 Gaps: 3
Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

Czaal47.Seq x Axiglcomplete.Con May 11, 2000 12:05 ..

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1 .....GCAGGAACCTTAT 12
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1101 CGCGTCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAACCTTAT 1150
      .      .      .      .      .      .      .      .      .      .
13 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 62
      |||||
1151 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 1200
      .      .      .      .      .      .      .      .      .      .
63 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTTCAGCTAGCTAGCTGCG 112
      |||||
1201 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTTCAGCTAGCTAGCTGCG 1250
      .      .      .      .      .      .      .      .      .      .
113 CCGTGACCACGCACATGACCGCAGTGCAGCGCGGGGCTGATCAAGGGAAAG 162
      |||||
1251 CCGTGACCACGCACATGACCGCAGTGCAGCGCGGGGCTGATCAAGGGAAAG 1300
      .      .      .      .      .      .      .      .      .      .
163 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 212
      |||||
1301 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 1350
      .      .      .      .      .      .      .      .      .      .
213 CGCTGGCTGCCGCCGCCGAGTTCGTTCGGTCTCCTCAGCAGCTCGGCTGGC 262
      |||||
1351 CGCTGGCTGCCGCCGCCGAGTTCGTTCGGTCTCCTCAGCAGCTCGGCTGGC 1400
      .      .      .      .      .      .      .      .      .      .
263 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 312
      |||||
1401 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 1450
      .      .      .      .      .      .      .      .      .      .
313 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 362
      |||||
1451 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 1500

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363 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAA.... 408
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1501 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAAGTGA 1550
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409 .....TGTACCCAGGAAGAAGAGGCTGG 431
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1601 CCCAAATCCGATCCGTGGTGTGTAGTGTACCCAGGAAGAAGAGGCTGG 1650
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432 TGGGGTGGCCCGCGGTGAAGTGC CGCGTAGGCGTAGCTGCGGCGGCGGG 481
|||||
1651 TGGGGTGGCCCGCGGTGAAGTGC CGCGTAGGCGTAGCTGCGGCGGCGGG 1700
.
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482 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 531
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1701 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 1750
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532 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 581
|||||
1751 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 1800
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582 TCCCTTCGGGTAACCAACA..... 600
|||||
1801 TCCCTTCGGGTAACCAACAAGGTGCGTACGTTCCCGGGCCGCGGCGAGCC 1850
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601 .....AG 602
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1951 CTCCCGGCACTTAACTTGGTCGCATATACTATTCTGTAACTCTGGCAG 2000
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603 ATCATGCAGAAGACGAGGTGGTGGTCTCGCACGAGCGCCCGCTCGCCAT 652
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2001 ATCATGCAGAAGACGAGGTGGTGGTCTCGCACGAGCGCCCGCTCGCCAT 2050
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653 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 702
|||||
2051 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 2100
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703 AGATGATGTGCCGTGGGA..... 720
|||||
2101 AGATGATGTGCCGTGGGAGTACGTATCAGTCACTACTACTGTCGTCGTGTA 2150
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721 .....GGTCTTTGTCAAGTCAGTG 739
|||||
2201 GAACTTAAAAACGACGTTGATTTCTTGTCAGGGTCTTTGTCAAGTCAGTG 2250
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740 AAGCGGCTCAAGATACTTGCGTAGCCGACGGTCGGCGCCTCAGAGACGTC 789
|||||
2251 AAGCGGCTCAAGATACTTGCGTAGCCGACGGTCGGCGCCTCAGAGACGTC 2300

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1800
 1750
 1700
 1650
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 1350
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 1200
 1150
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790 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 839
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2301 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 2350
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840 TCTGCGTAATAACGTTGTTTCTGTCCTGTGTGCCCCGTAGCAGTACGTACT 889
|||||
2351 TCTGCGTAATAACGTTGTTTCTGTCCTGTGTGCCCCGTAGCAGTACGTACT 2400
|||||
890 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 939
|||||
2401 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 2450
|||||
940 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCGT 989
|||||
2451 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCGT 2500
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|||||
2501 ACGGTATCGCTGGCGTCAGTGTGCGGGCAGCCTAGGTGATCTAAGCATAC 2550
|||||
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|||||
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|||||
1090 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 1139
|||||
2601 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 2650
|||||
1140 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAATAACTATTTAAC 1189
|||||
2651 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAATAACTATTTAAC 2700
|||||
1190 ACTGTTTCATCAATATATTTGATTTT..... 1214
|||||
2701 ACTGTTTCATCAATATATTTGATTTCAATAATTCATGGAGCTGACCTTGTG 2750

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Sequence Name	SEQ ID NO:	ATCC Deposit
Pioneer clone CZAAL47	1	PTA-2426
ZmAxig1 polypeptide	2	
Native ZmAxig1 promoter region	3	
Modified ZmAxig1 promoter region	4	PTA-2427
A632 full-length ZmAxig1, including SEQ ID No. 3	5	PTA-2426 PTA-2427
Primer 1, used for isolation of 5' flanking region	6	
Primer 2, used for isolation of 5' flanking region	7	
Primer 3, used for isolation of region spanning start codon	8	
Primer 4, used for isolation of region spanning start codon	9	
Primer 5, used for isolation of 5' region	10	
Oligonucleotide designed to remove clones having a poly-A tail but no cDNA	11	
Pioneer clone Cjlp181	12	
CuraGen fragment w0h051.7	13	
Primer 6, used to isolate the coding sequence and 3' region	14	
Primer 7, used to isolate the coding sequence and 3' region	15	
Modified ZmAxig1 promoter region with single-base deletion	16	PTA-2427
LEC1 transcriptional activator element	17	
LEC1 polynucleotides	18-20	
LEC1 polypeptide consensus sequence	21	

Figure 10. Representative polynucleotides and polypeptides of the present invention.

Experiment	Control	Ubi:LEC1	Axig1:LEC1
#1 3938.37	15%	63%	44%
#2 3938.79	4%	17%	20%
#3 3938.78	16%	17%	38%
#4 3938.34	2%	14%	13%

Figure 11. Transformation frequencies by LEC1 with two different promoters. Transformation frequencies were based on the percentage of plated embryos with one or more GFP positive/Bialaphos resistant colonies. All embryos were shot with Ubi:moPAT~GFP (a construct conferring Bialaphos resistance and GFP fluorescence) along with a LEC1 construct or a control DNA.